AMENDMENTS TO THE SPECIFICATION

Please amend paragraph 205, beginning at page 31, as follows:

Percent amino acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from ~~http://www.ncbi.nlm.nih.gov~~ the National Institutes of Health website or otherwise obtained from the National Institute of Health, Bethesda, MD. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.

Please amend paragraph 216 beginning at page 35, as follows:

Percent nucleic acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from ~~http://www.ncbi.nlm.nih.gov~~ the National Institutes of Health website or otherwise obtained from the National Institute of Health, Bethesda, MD. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.

Please amend paragraph 435, beginning at page 117, as follows:

When a positive colony was isolated, a portion of it was picked by a toothpick and diluted into sterile water (30 µl) in a 96 well plate. At this time, the positive colonies were either frozen and stored for subsequent analysis or immediately amplified. An aliquot of cells (5 µl) was used as a template for the PCR reaction in a 25 µl volume containing: 0.5 µl ~~Klentaq~~ KLENTAQ (a 5'-exo

minus N-terminal deletion of Taq DNA polymerase available from Clontech, Palo Alto, CA); 4.0 µl 10 mM dNTP's (Perkin Elmer-Cetus); 2.5 µl ~~Kentaq~~ KLENTAQ buffer (Clontech); 0.25 µl forward oligo 1; 0.25 µl reverse oligo 2; 12.5 µl distilled water. The sequence of the forward oligonucleotide 1 was:

Please amend paragraph 441, on page 119, as follows:

Following the PCR, an aliquot of the reaction (5 µl) was examined by agarose gel electrophoresis in a 1% agarose gel using a Tris-Borate-EDTA (TBE) buffering system as described by Sambrook et al., supra. Clones resulting in a single strong PCR product larger than 400 bp were further analyzed by DNA sequencing after purification with a 96 ~~Qiaquick~~ QIAQUICK PCR clean-up column (Qiagen Inc., Chatsworth, CA)

Please amend paragraph 475, beginning on page 129 as follows:

Twelve micrograms of the desired plasmid DNA is introduced into approximately 10 million CHO cells using commercially available transfection reagents ~~Superfect~~™ ~~(Quiagen)~~ SUPERFECT™ (Qiagen), ~~dosper~~™ DOSPER™ or ~~fugene~~™ FUGENE™ (Boehringer Mannheim). The cells are grown as described in Lucas et al., supra. Approximately 3 x 10^{-7} cells are frozen in an ampule for further growth and production as described below.

Please amend paragraph 489 beginning on page 131 as follows:

Recombinant baculovirus is generated by co-transfecting the above plasmid and ~~BaculoGold~~™ BACULOGOLD™ virus DNA (Pharmingen) into *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711) using ~~lipofectin~~ LIPOFECTIN cationic lipid (commercially available from GIBCO-BRL). After 4 - 5 days of incubation at 58°C, the released viruses are harvested and used for further amplifications. Viral infection and protein expression are performed as described by O'Reilley et al., Baculovirus expression vectors: A Laboratory Manual, Oxford: Oxford University Press (1994).

AMENDMENTS TO THE CLAIMS

1. (Currently Amended) An antibody that specifically binds to the polypeptide of ~~shown in FIG. 68 (~~SEQ ID NO: 68~~)~~.

2. (Original) The antibody of claim 1 which is a monoclonal antibody.

3. (Original) The antibody of claim 1 which is a humanized antibody.

4. (Original) The antibody of claim 1 which is an antibody fragment.

5. (Original) The antibody of claim 1 which is labeled.

6. (Canceled).

DELETION OF INVENTORS

Please correct the inventorship under 37 CFR §1.48(b) by removing the following inventors from the present application:

Dan L. Eaton

Ellen Filvaroff

Mary E. Gerritsen and

Colin K. Watanabe